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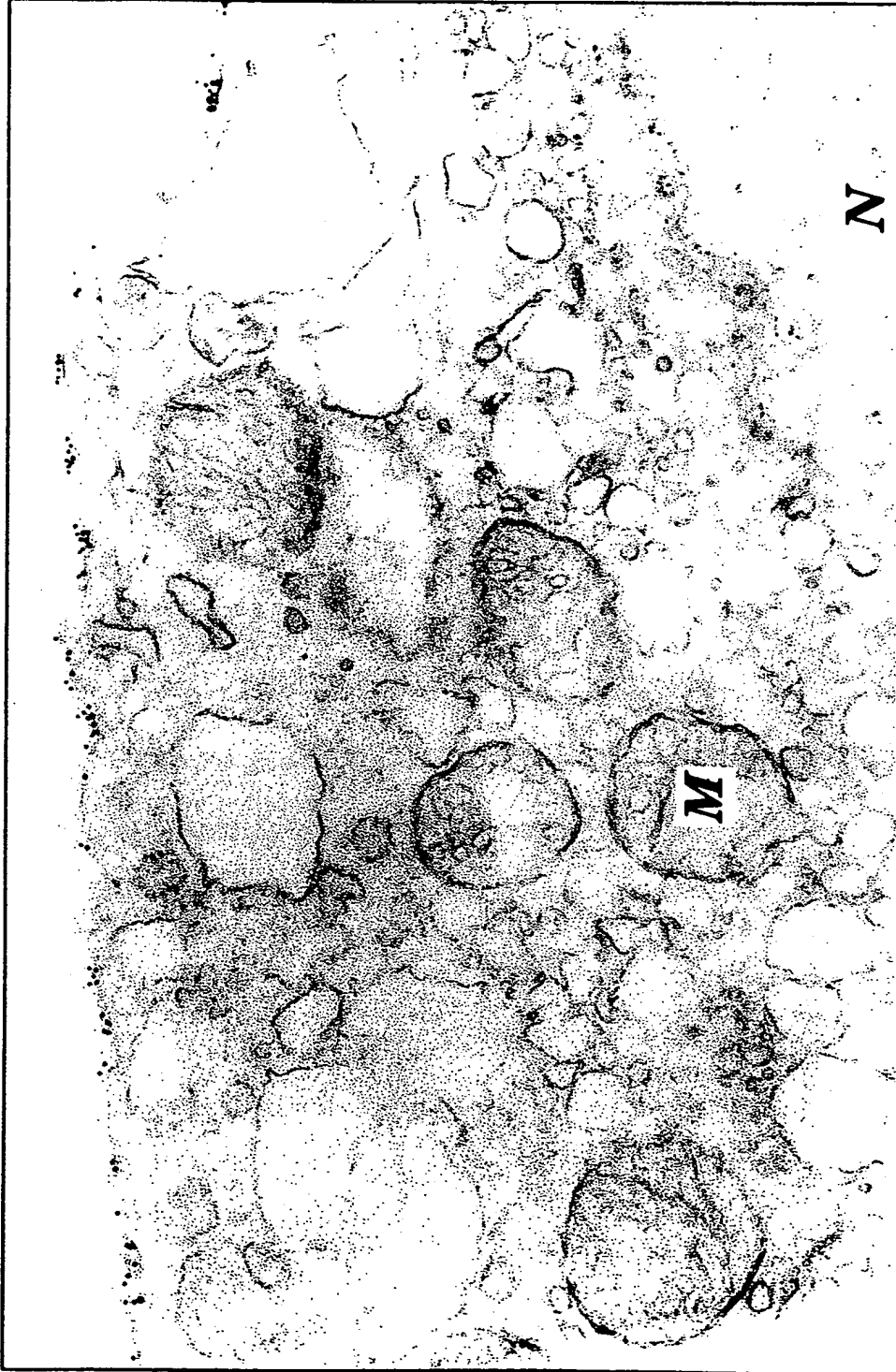


FIG. 1

FOOT-515000

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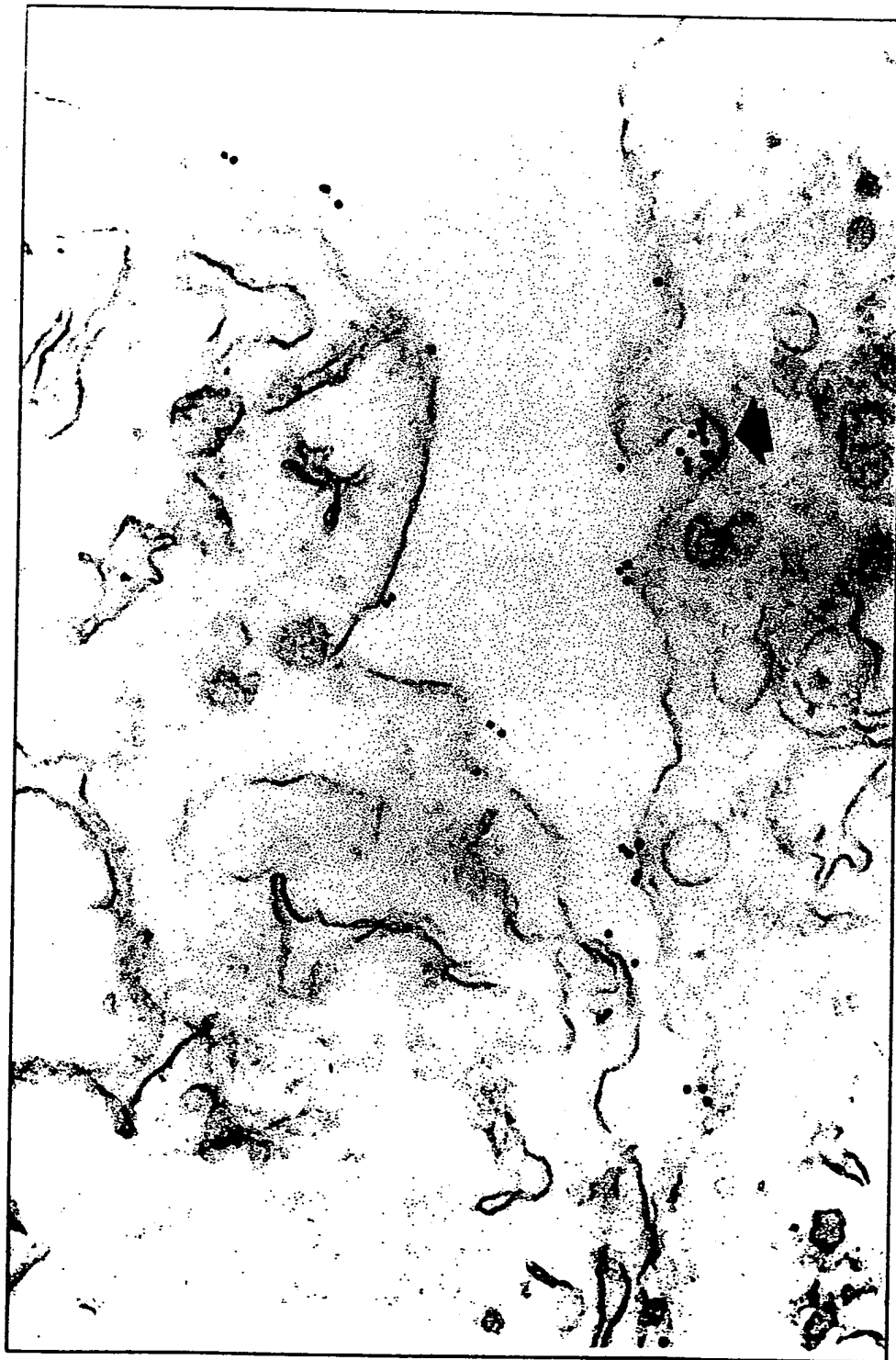


FIG. 2

FILE: SH50200

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FIG. 3

FIG. 3: SECTION

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FIG. 4

FIG. 4 - 5130000

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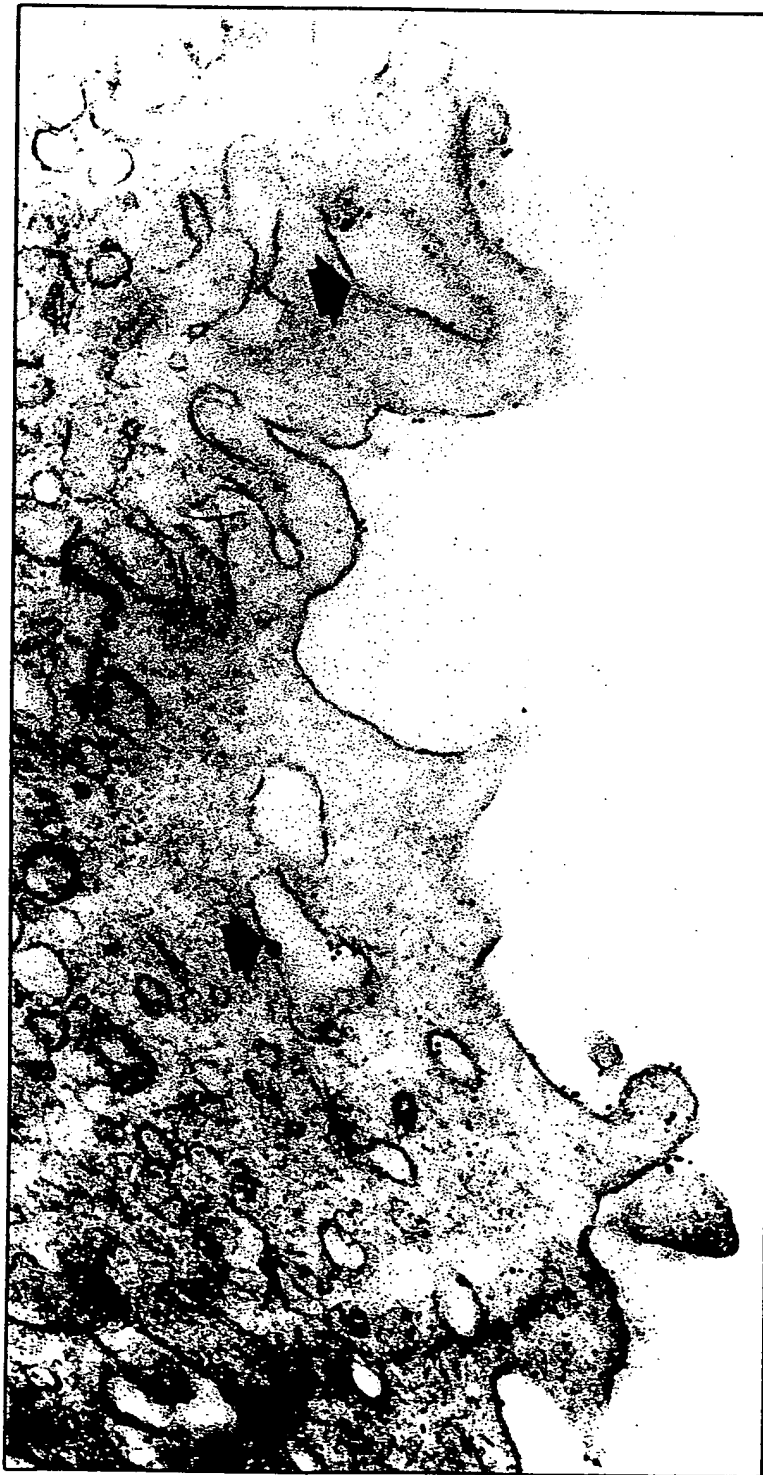


FIG. 5

FIG. 5

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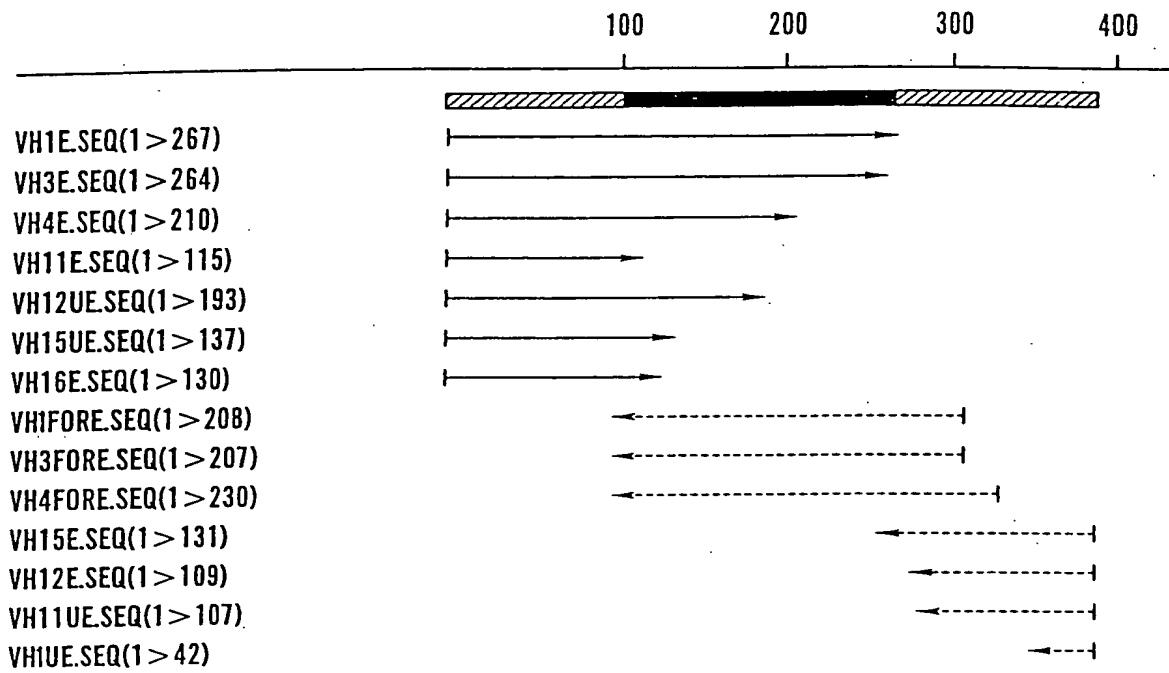


FIG. 6

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ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

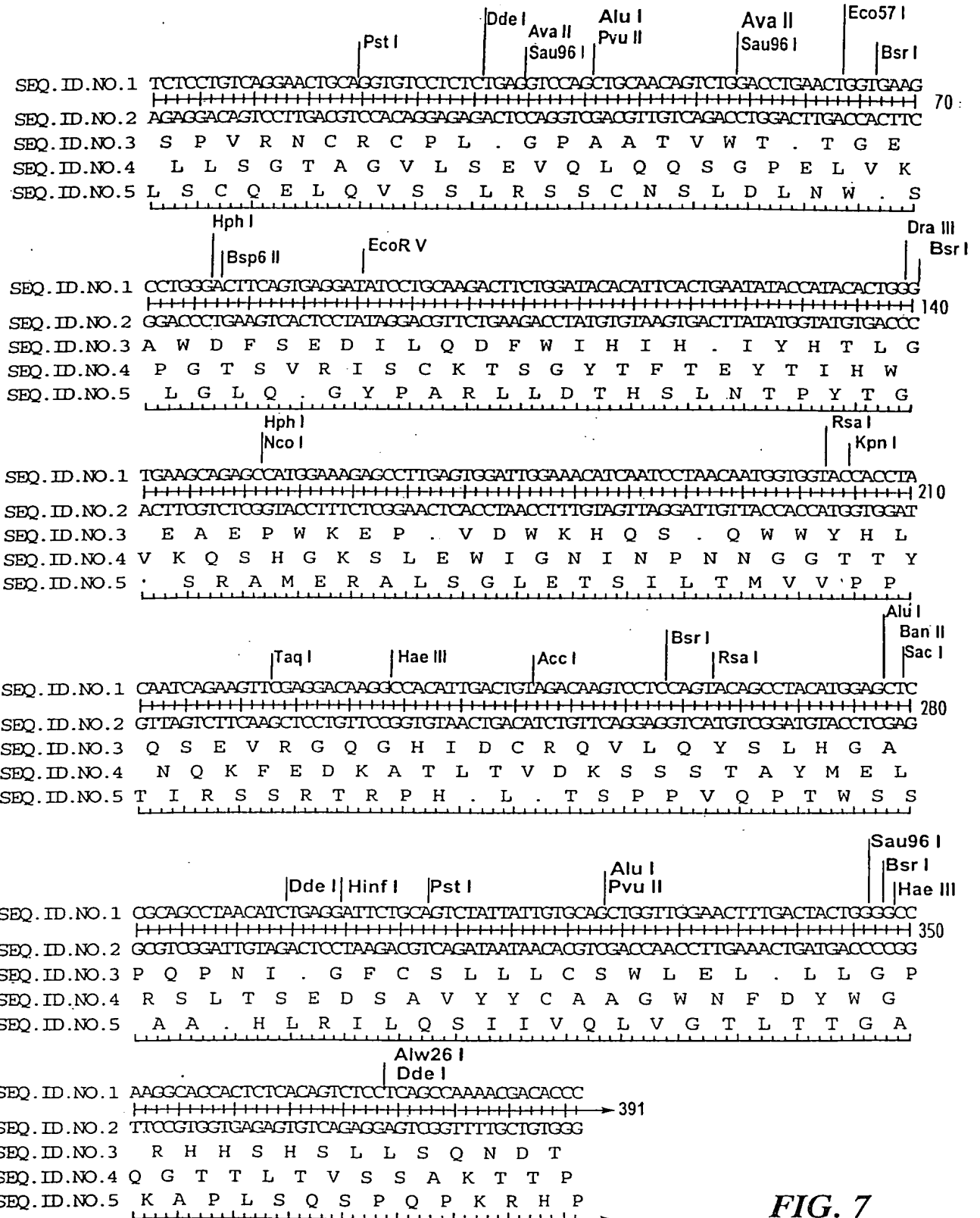


FIG. 7

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LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

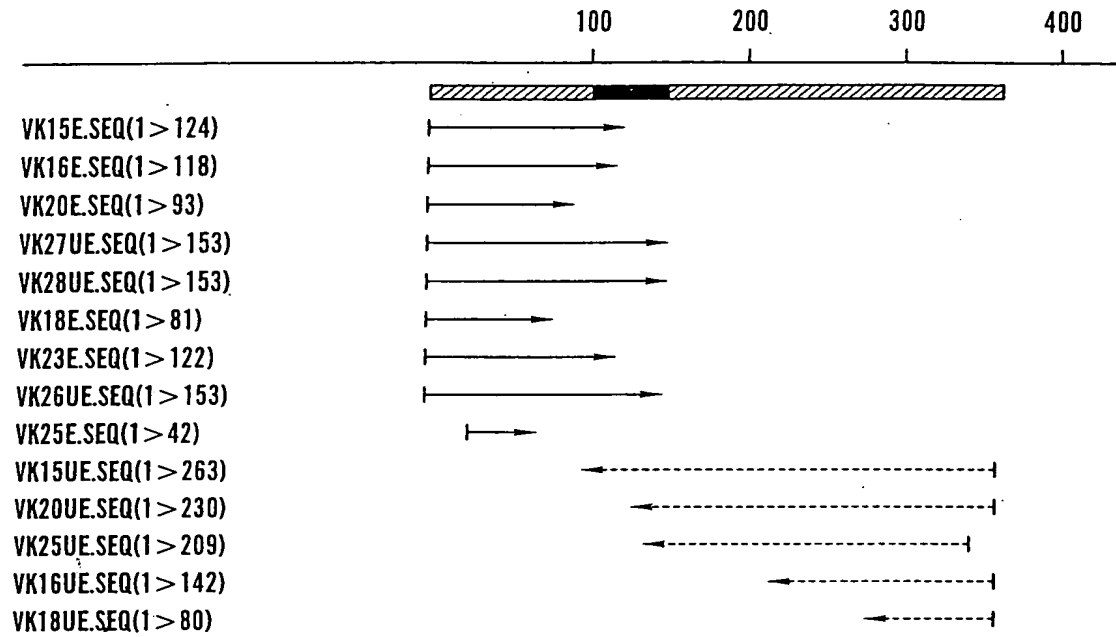
SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGT¹⁰SVRI²⁰SCKT³⁰SGYTF⁴⁰TEYTI⁵⁰-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y::WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFIDYMNINWVKQSPGKSLEWIGDINPGNGGTS
YNQKFEDKATLIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGIT
YNQKF.:KATLIVDKSSSTAYM:L.SLTSEDSAVYYCA G..FDYWGGIT
YNQKFKGKATLIVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT
⁶⁰⁷⁰⁸⁰⁹⁰¹⁰⁰¹¹⁰¹²⁰

LTVSS
:TVSS
VIVSS

FIG. 8

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**FIG. 9**

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ENZYMES: ALL 74 ENZYMES (NO FILTER):
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

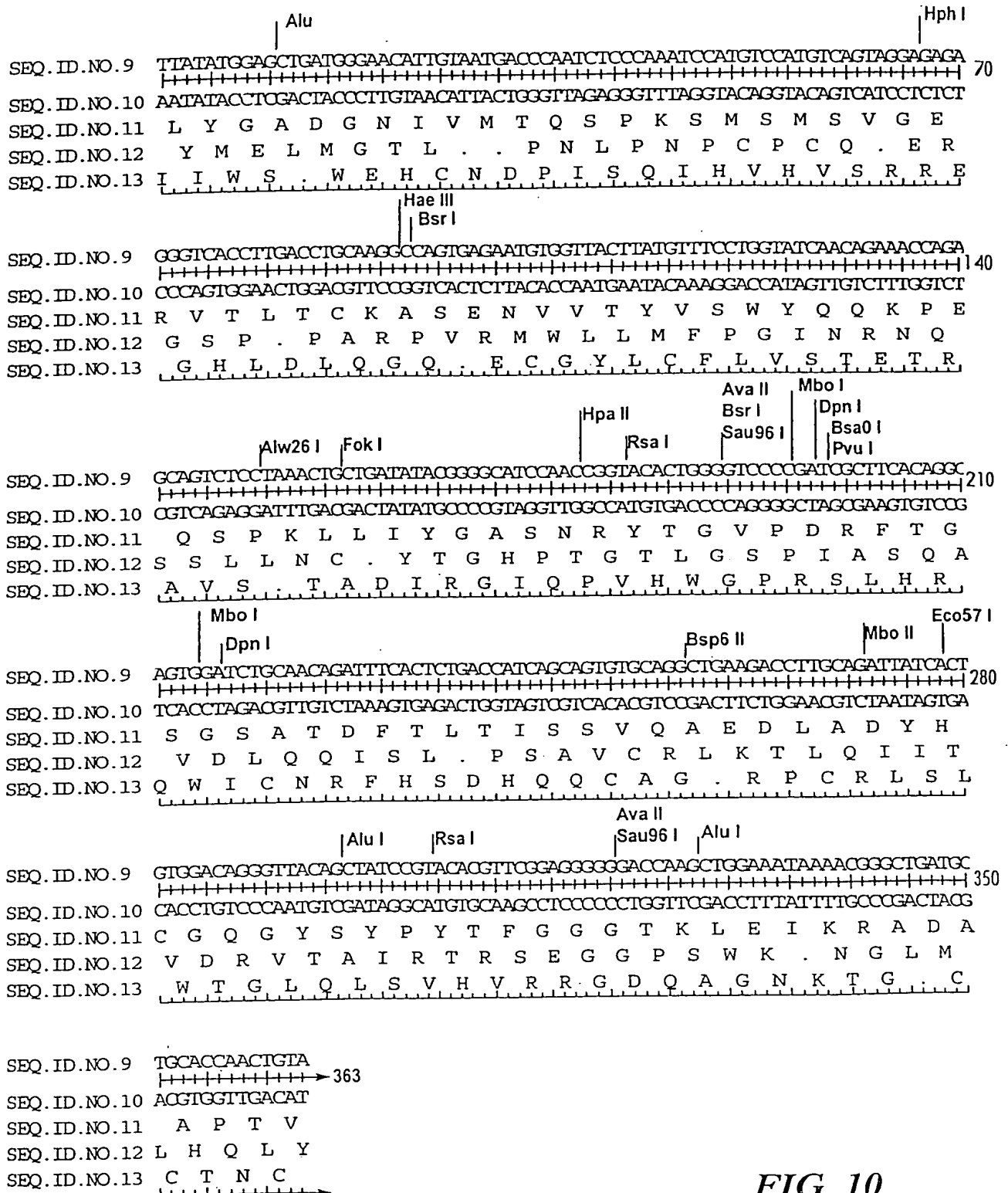


FIG. 10

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

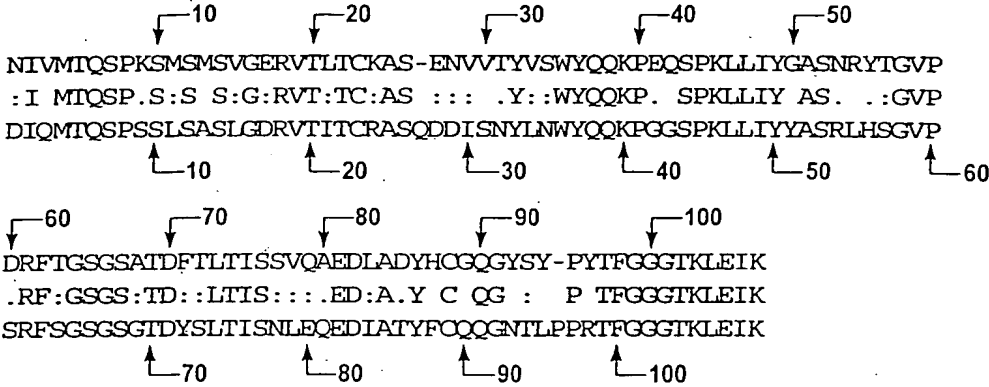


FIG. 11

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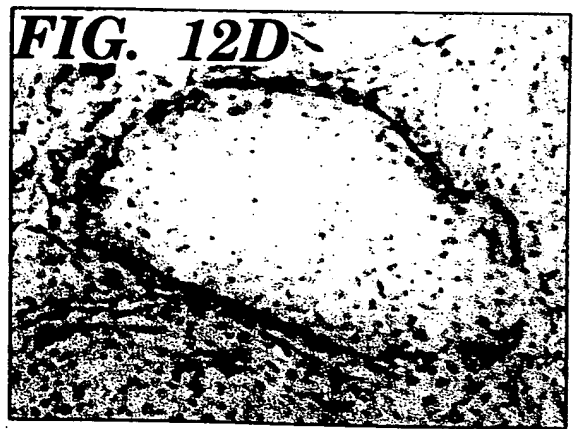
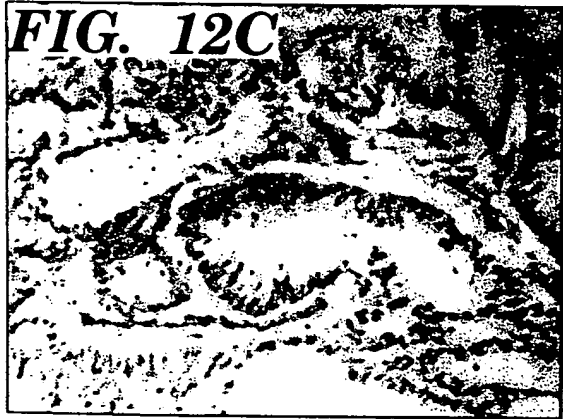


FIG. 12A